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> O <
O| |O  IntelliGenetics
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PEP - Polypeptide Analysis System
Version 5.4

Begin recording for user sdavid at 5-May-04 6:28am


PEP: hydropathicity

Hydropathicity: which set of hydropathicity values?
  ("H" = Hopp and Woods, "K" = Kyte and Doolittle): h
The window values from "hopp.win" have been loaded.

 The window values in this file were originally obtained from
 Hopp, T.P., and Woods, K.R.  "Prediction of protein antigenic
 determinants from amino acid sequences".  Proc. Natl. Acad. Sci.
 USA 78: 3824-3828, 1981.


There are no peptides currently loaded into pep.

Name of file to load (<CR>=cheu.pep):
      1. PEP1 ; Entered [sdavid 4-May-04 16:48]
      2. PEP2 ; Entered [sdavid 4-May-04 16:49]
      3. PEP3 ; Entered [sdavid 4-May-04 16:50]

Continuing...


    Name or number of the peptides to be analyzed (<CR> when done).

Peptide: 1
Peptide: 2
Peptide: 3
Peptide:


Do you wish to save the calculated results to a file? (<CR>=No) yes
File to store values in (<CR>=new.val): hopp.val
PEP1

A   -.500    B    .000    C  -1.000    D   3.000    E   3.000
F  -2.500    G    .000    H   -.500    I  -1.800    J    .000
K   3.000    L  -1.800    M  -1.300    N    .200    O    .000
P    .000    Q    .200    R   3.000    S    .300    T   -.400
U    .000    V  -1.500    W  -3.400    X    .000    Y  -2.300
Z    .000

Arithmetic Averaging:

Windowing average at residue i is calculated across 6 residues.

Maximum value: -.557143 at residue no. 9

Minimum value: -1.31111 at residue no. 2

                     -1               0                1
     -----------------!----------------!----------------!-----------------
  1                  ******************G
  2              **********************P
  3               *********************F
  4               *********************F
  5               *********************L
  6                 *******************A
  7                    ****************A
  8                         ***********S
  9                           *********V
     -----------------!----------------!----------------!-----------------
                     -1               0                1

PEP2

A   -.500    B    .000    C  -1.000    D   3.000    E   3.000
F  -2.500    G    .000    H   -.500    I  -1.800    J    .000
K   3.000    L  -1.800    M  -1.300    N    .200    O    .000
P    .000    Q    .200    R   3.000    S    .300    T   -.400
U    .000    V  -1.500    W  -3.400    X    .000    Y  -2.300
Z    .000

Arithmetic Averaging:

Windowing average at residue i is calculated across 6 residues.

Maximum value: .571429 at residue no. 10

Minimum value: -.15 at residue no. 4

                                      times 10^-1
         -5   -4   -3   -2   -1    0    1    2    3    4    5
     -----!----!----!----!----!----!----!----!----!----!----!-----
  1+                               R*******************
  2                                T*********
  3                                C*****
  4                         *******A
  5+                          *****H
  6                                P**********
  7                                G************
  8-                               E***************
  9+                               H**********************
 10                                A*****************************
     -----!----!----!----!----!----!----!----!----!----!----!-----
         -5   -4   -3   -2   -1    0    1    2    3    4    5
                                      times 10^-1

"+" or "-" after a residue number indicates a charged residue.

PEP3

A   -.500    B    .000    C  -1.000    D   3.000    E   3.000
F  -2.500    G    .000    H   -.500    I  -1.800    J    .000
K   3.000    L  -1.800    M  -1.300    N    .200    O    .000
P    .000    Q    .200    R   3.000    S    .300    T   -.400
U    .000    V  -1.500    W  -3.400    X    .000    Y  -2.300
Z    .000

Arithmetic Averaging:

Windowing average at residue i is calculated across 6 residues.

Maximum value: -.263636 at residue no. 7

Minimum value: -.728571 at residue no. 1

                                      times 10^-1
        -7  -6  -5  -4  -3  -2  -1   0   1   2   3   4   5   6   7
     ----!---!---!---!---!---!---!---!---!---!---!---!---!---!---!----
  1     *****************************L
  2          ************************P
  3              ********************A
  4+                      ***********H
  5                        **********G
  6                    **************P
  7                        **********S
  8                        **********L
  9                     *************S
     ----!---!---!---!---!---!---!---!---!---!---!---!---!---!---!----
        -7  -6  -5  -4  -3  -2  -1   0   1   2   3   4   5   6   7
                                      times 10^-1

"+" or "-" after a residue number indicates a charged residue.
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```
PEP1 1 9
    Residue       Value
    A   Ala       -.5
    B   Asx       0
    C   Cys       -1
    D   Asp       3
    E   Glu       3
    F   Phe       -2.5
    G   Gly       0
    H   His       -.5
    I   Ile       -1.8
    J   N/A       0
    K   Lys       3
    L   Leu       -1.8
    M   Met       -1.3
    N   Asn       .2
    O   N/A       0
    P   Pro       0
    Q   Gln       .2
    R   Arg       3
    S   Ser       .3
    T   Thr       -.4
    U   N/A       0
    V   Val       -1.5
    W   Trp       -3.4
    X   Xaa       0
    Y   Tyr       -2.3
    Z   Glx       0
Window-Size = 6

Weight Values = 1 1 1 1 1 1 1
                    ^

   1    G/Gly   -1.0714
   2    P/Pro   -1.3111
   3    F/Phe   -1.2818
   4    F/Phe   -1.2583
   5    L/Leu   -1.2750
   6    A/Ala   -1.1667
   7    A/Ala    -.9545
   8    S/Ser    -.6889
   9    V/Val    -.5571
PEP2 1 10
    Residue       Value
    A   Ala       -.5
    B   Asx       0
    C   Cys       -1
    D   Asp       3
    E   Glu       3
    F   Phe       -2.5
    G   Gly       0
    H   His       -.5
    I   Ile       -1.8
    J   N/A       0
    K   Lys       3
    L   Leu       -1.8
    M   Met       -1.3
    N   Asn       .2
    O   N/A       0
    P   Pro       0
    Q   Gln       .2
    R   Arg       3
    S   Ser       .3
    T   Thr       -.4
    U   N/A       0
    V   Val       -1.5
    W   Trp       -3.4
    X   Xaa       0
    Y   Tyr       -2.3
    Z   Glx       0
Window-Size = 6

Weight Values = 1 1 1 1 1 1 1
                          ^

   1    R/Arg     .3857
   2    T/Thr     .1889
   3    C/Cys     .1091
   4    A/Ala    -.1500
   5    H/His    -.1167
   6    P/Pro     .2083
   7    G/Gly     .2500
   8    E/Glu     .3182
   9    H/His     .4444
  10    A/Ala     .5714
PEP3 1 9
    Residue       Value
    A   Ala       -.5
    B   Asx       0
    C   Cys       -1
    D   Asp       3
    E   Glu       3
    F   Phe       -2.5
    G   Gly       0
    H   His       -.5
    I   Ile       -1.8
    J   N/A       0
    K   Lys       3
    L   Leu       -1.8
    M   Met       -1.3
    N   Asn       .2
    O   N/A       0
    P   Pro       0
    Q   Gln       .2
    R   Arg       3
    S   Ser       .3
    T   Thr       -.4
    U   N/A       0
    V   Val       -1.5
    W   Trp       -3.4
    X   Xaa       0
    Y   Tyr       -2.3
    Z   Glx       0
Window-Size = 6

Weight Values = 1 1 1 1 1 1 1
                    ^

   1    L/Leu    -.7286
   2    P/Pro    -.6222
   3    A/Ala    -.5091
   4    H/His    -.2917
   5    G/Gly    -.2667
   6    P/Pro    -.3500
   7    S/Ser    -.2636
   8    L/Leu    -.2667
   9    S/Ser    -.3429
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> O <
O| |O  IntelliGenetics
> O <

PEP - Polypeptide Analysis System
Version 5.4

Begin recording for user sdavid at 5-May-04 6:33am


PEP: hydro

Hydropathicity: which set of hydropathicity values?
  ("H" = Hopp and Woods, "K" = Kyte and Doolittle): k
The window values from "kyte.win" have been loaded.

 The window values in this file were originally obtained from
 Kyte, J., and R. F. Doolittle.  "A Method for Displaying the
 Hydropathic Character of a Protein."  J. Mol. Biol. 157: 105-132, 1982.


There are no peptides currently loaded into pep.

Name of file to load (<CR>=cheu.pep):
      1. PEP1 ; Entered [sdavid 4-May-04 16:48]
      2. PEP2 ; Entered [sdavid 4-May-04 16:49]
      3. PEP3 ; Entered [sdavid 4-May-04 16:50]

Continuing...

    Name or number of the peptides to be analyzed (<CR> when done).

Peptide: 1
Peptide: 2
Peptide: 3
Peptide:


Do you wish to save the calculated results to a file? (<CR>=No) yes
File to store values in (<CR>=new.val): kyte.val

File "kyte.val" already exists.  (R)eplace, (A)ppend, or (N)ew filename? r
PEP1

A   1.800    B  -3.500    C   2.500    D  -3.500    E  -3.500
F   2.800    G   -.400    H  -3.200    I   4.500    J    .000
K  -3.900    L   3.800    M   1.900    N  -3.500    O    .000
P  -1.600    Q  -3.500    R  -4.500    S   -.800    T   -.700
U    .000    V   4.200    W   -.900    X    .000    Y  -1.300
Z  -3.500

Arithmetic Averaging:

Windowing average at residue i is calculated across 6 residues.

Maximum value: 2.21818 at residue no. 7

Minimum value: .628571 at residue no. 1

               -2         -1          0          1          2
     -----------!----------!----------!----------!----------!-----------
  1                                   G******
  2                                   P************
  3                                   F***************
  4                                   F*****************
  5                                   L*******************
  6                                   A*********************
  7                                   A**********************
  8                                   S*******************
  9                                   V******************

     -----------!----------!----------!----------!----------!-----------
               -2         -1          0          1          2

PEP2

A   1.800    B  -3.500    C   2.500    D  -3.500    E  -3.500
F   2.800    G   -.400    H  -3.200    I   4.500    J    .000
K  -3.900    L   3.800    M   1.900    N  -3.500    O    .000
P  -1.600    Q  -3.500    R  -4.500    S   -.800    T   -.700
U    .000    V   4.200    W   -.900    X    .000    Y  -1.300
Z  -3.500

Arithmetic Averaging:

Windowing average at residue i is calculated across 6 residues.

Maximum value: -.5 at residue no. 5

Minimum value: -1.68333 at residue no. 7

                       -1               0               1
     -----------------!----------------!----------------!-----------------
  1+                          ********R
  2                          *********T
  3                    ***************C
  4                         **********A
  5+                          ********H
  6               ********************P
  7       ****************************G
  8-        **************************E
  9+           ***********************H
 10           ************************A
     -----------------!----------------!----------------!-----------------
                       -1               0               1

"+" or "-" after a residue number indicates a charged residue.

PEP3

A   1.800    B  -3.500    C   2.500    D  -3.500    E  -3.500
F   2.800    G   -.400    H  -3.200    I   4.500    J    .000
K  -3.900    L   3.800    M   1.900    N  -3.500    O    .000
P  -1.600    Q  -3.500    R  -4.500    S   -.800    T   -.700
U    .000    V   4.200    W   -.900    X    .000    Y  -1.300
Z  -3.500

Arithmetic Averaging:

Windowing average at residue i is calculated across 6 residues.

Maximum value: .685714 at residue no. 1

Minimum value: -.583333 at residue no. 4

                                     times 10^-1
          -6   -5   -4   -3   -2   -1    0    1    2    3    4    5    6
     -----!----!----!----!----!----!----!----!----!----!----!----!----!-----
  1                                     L**********************************
  2                                     P******
  3                                  ***A
  4+      *****************************H
  5           *************************G
  6                      **************P
  7                        ************S
  8                                     L****
  9                                     S******************
     -----!----!----!----!----!----!----!----!----!----!----!----!----!-----
          -6   -5   -4   -3   -2   -1    0    1    2    3    4    5    6
                                     times 10^-1

"+" or "-" after a residue number indicates a charged residue.
```

PEP1 1 9

Residue		Value
A	Ala	1.8
B	Asx	-3.5
C	Cys	2.5
D	Asp	-3.5
E	Glu	-3.5
F	Phe	2.8
G	Gly	-.4
H	His	-3.2
I	Ile	4.5
J	N/A	0
K	Lys	-3.9
L	Leu	3.8
M	Met	1.9
N	Asn	-3.5
O	N/A	0
P	Pro	-1.6
Q	Gln	-3.5
R	Arg	-4.5
S	Ser	-.8
T	Thr	-.7
U	N/A	0
V	Val	4.2
W	Trp	-.9
X	Xaa	0
Y	Tyr	-1.3
Z	Glx	-3.5

Window-Size = 6

Weight Values = 1 1 1 1 1 1 1

1	G/Gly	.6286
2	P/Pro	1.2222
3	F/Phe	1.5091
4	F/Phe	1.7167
5	L/Leu	1.9667
6	A/Ala	2.1500
7	A/Ala	2.2182
8	S/Ser	1.9778
9	V/Val	1.7429

PEP2 1 10

Residue		Value
A	Ala	1.8
B	Asx	-3.5
C	Cys	2.5
D	Asp	-3.5
E	Glu	-3.5
F	Phe	2.8
G	Gly	-.4
H	His	-3.2
I	Ile	4.5
J	N/A	0
K	Lys	-3.9
L	Leu	3.8
M	Met	1.9
N	Asn	-3.5
O	N/A	0
P	Pro	-1.6
Q	Gln	-3.5
R	Arg	-4.5
S	Ser	-.8
T	Thr	-.7
U	N/A	0
V	Val	4.2
W	Trp	-.9
X	Xaa	0
Y	Tyr	-1.3
Z	Glx	-3.5

Window-Size = 6

Weight Values = 1 1 1 1 1 1 1

1	R/Arg	-.5143
2	T/Thr	-.5556
3	C/Cys	-.8909
4	A/Ala	-.6083
5	H/His	-.5000
6	P/Pro	-1.2083
7	G/Gly	-1.6833
8	E/Glu	-1.5455
9	H/His	-1.3556
10	A/Ala	-1.4571

PEP3 1 9

Residue		Value
A	Ala	1.8
B	Asx	-3.5
C	Cys	2.5
D	Asp	-3.5
E	Glu	-3.5
F	Phe	2.8
G	Gly	-.4
H	His	-3.2
I	Ile	4.5
J	N/A	0
K	Lys	-3.9
L	Leu	3.8
M	Met	1.9
N	Asn	-3.5
O	N/A	0
P	Pro	-1.6
Q	Gln	-3.5
R	Arg	-4.5
S	Ser	-.8
T	Thr	-.7
U	N/A	0
V	Val	4.2
W	Trp	-.9
X	Xaa	0
Y	Tyr	-1.3
Z	Glx	-3.5

Window-Size = 6

Weight Values = 1 1 1 1 1 1 1

1	L/Leu	.6857
2	P/Pro	.1333
3	A/Ala	-.0727
4	H/His	-.5833
5	G/Gly	-.5167
6	P/Pro	-.2833
7	S/Ser	-.2545
8	L/Leu	.0889
9	S/Ser	.4000